

Package: GenoTriplo (via r-universe)

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Type Package

Title Genotyping Triploids/Tetraploids (or Diploids) from Luminescence Data

Version 2.2.2

Description Genotyping of triploid individuals from luminescence data (marker probeset A and B). Works also for diploids and tetraploids. Three main functions: `Create_Dataset_from_file()` to build dataset ; `Clustering_parallele_from_dir()` that regroups individuals with a same genotype based on proximity and `Genotyping_parallele_from_dir()` that assigns a genotype to each cluster. For Shiny interface use: `launch_GenoShiny()`.

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Clustering	<i>Clustering function</i>
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Description

Clustering function to run clustering with no parallelization process nor auto save

Usage

```
Clustering(data_clustering, nb_clust_possible, n_iter = 5, Dmin = 0.28)
```

Arguments

- data_clustering dataset with Contrast and SigStren for each individuals (as SampleName) and each markers (as MarkerName)
- nb_clust_possible number of cluster possible (ploidy+1)
- n_iter number of iterations to perform for clustering
- Dmin minimal distance between two clusters

Value

list of results of clustering

Examples

```
## Not run:
file.create = system.file("extdata/output_create/1", "1_1_to_clust.Rdata", package = "GenoTriplo")
load(file.create)
ploidy=3
Clustering(data_clustering=data_clustering,nb_clust_possible=ploidy+1)

## End(Not run)
```

Clustering_from_dir	<i>Clustering function from directory</i>
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Description

Clustering function to run clustering with no parallelization process and autosave

Usage

```
Clustering_from_dir(  
  dir_from_create,  
  new.dir = NULL,  
  ploidy,  
  n_iter = 5,  
  Dmin = 0.28  
)
```

Arguments

dir_from_create	directory of the file to clusterize.
new.dir	new directory name for saving in './output_clustering'
ploidy	ploidy of individuals
n_iter	number of iterations to perform for clustering
Dmin	minimal distance between two clusters

Value

Autosave of the results in new.dir

Examples

```
## Not run:  
dir.create = system.file("extdata/output_create/1", package = "GenoTriplo")  
ploidy = 3  
Clustering_from_dir(dir_from_create=dir.create,ploidy=ploidy)  
  
## End(Not run)
```

Clustering_from_file *Clustering function from file*

Description

Clustering function to run clustering with no parallelization process and autosave Used by Clustering_from_dir. Shouldn't be used else.

Usage

```
Clustering_from_file(  
  dirname,  
  filename,  
  ploidy,  
  n_iter = 5,  
  Dmin = 0.28,  
  new.dir = NULL  
)
```

Arguments

dirname	directory of the file to clusterize.
filename	filename of the data to clusterize
ploidy	ploidy of individuals
n_iter	number of iterations to perform for clustering
Dmin	minimal distance between two clusters
new.dir	new directory name for saving

Value

Autosave of the results

Examples

```
## Not run:  
dir.create = system.file("extdata/output_create/1", package = "GenoTriplo")  
file.create = system.file("extdata/output_create/1", "1_1_to_clust.Rdata", package = "GenoTriplo")  
ploidy=3  
Clustering_from_file(dirname=dir.create,filename=file.create,ploidy=ploidy)  
  
## End(Not run)
```

`Clustering_parallele_from_dir`*Launch parallel clustering from directory*

Description

Launch the clustering phase in parallel from the dataset with SampleName, Contrast and SigStren for each markers (MarkerName).

Usage

```
Clustering_parallele_from_dir(  
  dir_from_create,  
  new.dir = NULL,  
  ploidy,  
  n_iter = 5,  
  Dmin = 0.28,  
  n_core = 1  
)
```

Arguments

<code>dir_from_create</code>	directory name with dataset files saved in './output_create'
<code>new.dir</code>	directory name where output is saved as in './output_clustering'
<code>ploidy</code>	ploidy of individuals
<code>n_iter</code>	number of iterations of clustering
<code>Dmin</code>	threshold distance between two clusters
<code>n_core</code>	number of cores used for parallelization

Value

the result of clustering or automatically save a list of objects if a saving name has been provided

Examples

```
## Not run:  
dir.create = system.file("extdata/output_create/1", package = "GenoTriplo")  
Clustering_parallele_from_dir(dir_from_create=dir.create,ploidy=3)  
  
## End(Not run)
```

Create_Dataset_from_file

Create dataset from filename in appropriate format

Description

Create SigStren and Contrast variables from luminescence values of probeset A and B of each markers and return a dataframe to be used for clustering or save the result if a saving name is given

Usage

```
Create_Dataset_from_file(
  filename = "./AxiomGT1.summary.txt",
  dir.name = NULL,
  indiv_name = NULL,
  marker_name = NULL,
  n_marker_chunk = 4000,
  simplify.names = TRUE
)
```

Arguments

filename	filename from AXAS : AxiomGT1.summary.txt
dir.name	saving name (the number of the chunk and _to_clust is automatically added)
indiv_name	vector with name of individuals to keep
marker_name	vector with name of marker to keep
n_marker_chunk	number of lines by chunk (have to be even as markers goes by pair)
simplify.names	Samplenames might be like so : IndivXX_a1_a1.CEL (if from Axiom) -> allows to select only IndivXX as SampleName

Value

save file in ./output_create/dir.name as k_to_clust.Rdata with k the chunk number.

Examples

```
## Not run:
filepath = system.file("extdata", "AxiomGT1.summary_examples.txt", package = "GenoTriplo")
Create_Dataset_from_file(filename=filepath)

## End(Not run)
```

create_genofiles	<i>Create files of genotype and indiv/marker stats from genotype .Rdata files</i>
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Description

Create files of genotype and indiv/marker stats from genotype .Rdata files

Usage

```
create_genofiles(dir.name.save, new.dir, ploidy, corres_ATCG = NULL)
```

Arguments

dir.name.save	directory with .Rdata files with genotype
new.dir	new directory for saving files
ploidy	ploidy of the population
corres_ATCG	dataframe with correspondance between Allele_A/Allele_B to ATCG

Value

names of the indivCR and markerCR files

Examples

```
## Not run:  
ploidy = 3  
dir.name.save = system.file("extdata/output_genotyping/1", package = "GenoTriplo")  
new.dir = "1"  
create_genofiles(dir.name.save=dir.name.save,new.dir=new.dir,ploidy=ploidy)  
  
## End(Not run)
```

Genotyping_from_file	<i>Run genotyping from file</i>
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Description

Run genotyping from file

Usage

```

Genotyping_from_file(
  dirname,
  filename,
  new.dir = NULL,
  ploidy,
  SeuilNoCall = 0,
  SeuilNbSD = 2.8,
  SeuilSD = 0.28,
  cr_marker = 0.97,
  fld_marker = 3.4,
  hetso_marker = -0.3,
  same.pop = TRUE,
  tryEqHW = TRUE
)

```

Arguments

dirname	name of the directory where the file is
filename	name of the file with the data for genotyping
new.dir	new directory name for saving
ploidy	ploidy of individuals
SeuilNoCall	threshold of the probability of belonging to a cluster
SeuilNbSD	threshold for the distance between an individuals and his cluster ($x = \text{Contrast}$)
SeuilSD	threshold for the standard deviation of a cluster ($\text{SeuilSD} * (1 + 0.5 * \text{abs}(\text{mean_contrast_cluster}))$)
cr_marker	call rate threshold
fld_marker	FLD threshold
hetso_marker	HetSO threshold
same.pop	Boolean : are individuals from a same population
tryEqHW	Only if same.pop==TRUE else ignore. If TRUE, will delete cluster that shouldn't happen under H-W equilibrium (heterozygote with less individuals than both homozygote in triploid for example). Additionnaly, the cluster should contain less than 5% of the individuals. Else it stays.

Value

Void. Save the results

Examples

```

## Not run:
ploidy=3
dir_from_clustering=system.file("extdata/output_clustering/1", package = "GenoTriplo")
file_from_clustering=system.file(
  "extdata/output_clustering/1",
  "1_1_to_genos.Rdata", package = "GenoTriplo")

```

```
Genotyping_from_file(dirname=dir_from_clustering,ploidy=ploidy,filename=file_from_clustering)

## End(Not run)
```

Genotyping_parallelele_from_dir

Launch genotyping phase in parallel from directory

Description

Function that launch the genotyping phase from the dataset with SampleName, Contrast and SigStren for each markers and the result of the 'Run_clustering' function.

Usage

```
Genotyping_parallelele_from_dir(
  dir_from_clustering,
  new.dir = NULL,
  ploidy,
  SeuilNoCall = 0,
  SeuilNbSD = 2.8,
  SeuilSD = 0.28,
  n_core = 1,
  corres_ATCG = NULL,
  same.pop = TRUE,
  cr_marker = 0.97,
  fld_marker = 3.4,
  hetso_marker = -0.3,
  tryEqHW = TRUE
)
```

Arguments

dir_from_clustering	directory with files from clustering phase
new.dir	name of the new directory for saving results in './output_genotyping'
ploidy	ploidy of individuals
SeuilNoCall	threshold of the probability of belonging to a cluster
SeuilNbSD	threshold for the distance between an individuals and his cluster (x=Contrast)
SeuilSD	threshold for the standard deviation of a cluster (SeuilSD*(1+0.5*abs(mean_contrast_cluster)))
n_core	number of cores used for parallelization
corres_ATCG	dataframe with the correspondence between A/B of AXAS and A/T/C/G (three columns : probeset_id, Allele_A, Allele_B)
same.pop	Boolean : are individuals from a same population
cr_marker	call rate threshold

fld_marker	FLD threshold
hetso_marker	HetSO threshold
tryEqHW	Only if same.pop==TRUE else ignore. If TRUE, will delete cluster that shouldn't happen under H-W equilibrium (heterozygote with less individuals than both homozygote in triploid for example). Additionnaly, the cluster should contain less than 5% of the individuals. Else it stays.

Value

Void. Save the results.

Examples

```
## Not run:
ploidy=3
dir_from_clustering=system.file("extdata/output_clustering/1", package = "GenoTriplo")
Genotyping_parallels_from_dir(dir_from_clustering=dir_from_clustering,ploidy=ploidy)

## End(Not run)
```

launch_GenoShiny

Shiny App for genotyping

Description

Launch a shiny interface to use GenoTriplo. Really easy to use and user friendly, this will help you gain time !

Usage

```
launch_GenoShiny()
```

Value

void : most results are automatically saved

Examples

```
## Not run:
launch_GenoShiny()

## End(Not run)
```

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